In the Claims

1. (original) A method for increasing or decreasing nitrogen metabolism in plant cells, said method comprising the steps of transforming a plant cell with a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity, and culturing said cell whereby descendant cells are produced which comprise said polynucleotide and express said polynucleotide, whereby nitrogen metabolism is increased or decreased as compared to nitrogen metabolism of untransformed plant cells.

2. (original) The method of claim 1, further comprising the step of regenerating a plant from said descendant cells.

3. (original) The method of claim 1, wherein said increasing nitrogen metabolism comprises increasing the assimilation of inorganic nitrogen into organic nitrogen.

4. (original) The method of claim 1, wherein said polypeptide is selected from the group consisting of an alpha subunit of glutamate dehydrogenase, a beta subunit of glutamate dehydrogenase, and fragments of said alpha subunit or said beta subunit which exhibit glutamate dehydrogenase activity.

5. (original) The method of claim 1, wherein said polynucleotide is operably linked to a polynucleotide encoding a chloroplast transit peptide.

6. (original) The method of claim 5, wherein the chloroplast transit peptide comprises SEQ ID NO: 5 or SEQ ID NO: 6, or a fragment thereof of sufficient length to exhibit chloroplast transit activity.

7. (original) The method of claim 1, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 24, SEQ ID NO: 26, and fragments of any of the foregoing of sufficient length to exhibit α-GDH or β-GDH activity.

8. (original) The method of claim 1, wherein said polynucleotide is operably linked to a plant polyadenylation sequence.

9. (original) The method of claim 1, further comprising, prior to said transforming step, engineering said polynucleotide to maximize expression in said plant cell, said engineering comprising determining favored codon usage in said plant cell and altering said polynucleotide by increasing the frequency of favored codons.

10. (original) A method of increasing biomass, increasing total protein in seeds and plants, increasing total carbon/nitrogen level, increasing grain density, or increasing plant yield comprising culturing a plant comprising transgenic cells that comprise a polynucleotide encoding a polypeptide having glutamate dehydrogenase activity under conditions where said polynucleotide is expressed in said cells, whereby biomass is increased, total protein in seeds and plants is increased, total carbon/nitrogen level is increased, grain density is increased, or plant yield is increased, as compared to an untransformed plant.

12. (original) The method of claim 10, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 24, SEQ ID NO: 26, and fragments thereof having glutamate dehydrogenase activity.

13. (original) A plant produced by the method of claim 2, said plant having increased or decreased nitrogen metabolism as compared to an untransformed plant.

14. (original) A descendant of the plant of claim 13, said descendant comprising cells expressing said polypeptide.

15. (original) A recombinant DNA molecule comprising a constitutive promoter operably linked to a sequence encoding a polypeptide, wherein said polypeptide comprises a chloroplast transit peptide operably linked to a NADP-GDH polypeptide, and wherein said sequence encoding a polypeptide is operably linked to a transcriptional termination region.

16. (original) The recombinant DNA of claim 15, wherein said NADP-GDH polypeptide is a bacterial polypeptide.

17. (original) A transgenic plant comprising an expression cassette having:

a transcription initiation region functional in a plant cell of said transgenic plant; and

a DNA sequence that encodes a NADP-GDH enzyme in said plant cell;

whereby said transgenic plant evidences detectable increases in NADP-GDH enzyme activity when compared to non-transgenic plants by having an increased yield relative to that of non-transgenic plants.

18. (original) The transgenic plant of claim 17, wherein said NADP-GDH enzyme is a bacterial enzyme.

19. (original) The transgenic plant according to claim 18, wherein said plant is a dicot.

20. (original) The transgenic plant according to claim 18, wherein said plant is a monocot.

21. (original) The transgenic plant according to claim 20, wherein said plant is Zea mays.

22. (original) Transgenic plant cells comprising an expression cassette having:

a transcription initiation region functional in said transgenic plant cells;

a DNA sequence that encodes an NADP-GDH enzyme in said transgenic plant cells; and

a transcription termination region functional in said transgenic plant cells; wherein said expression cassette imparts increased yield to a transgenic plant resulting from the transgenic plant cells relative to wild-type plants resulting from wild-type plant cells.

23. (original) The transgenic cells according to claim 22, wherein at least one of said transcription initiation region and said transcription termination region is not naturally associated with said sequence.

24. (original) The transgenic cells according to claim 22, wherein said NADP-GDH enzyme is a bacterial enzyme.

25. (original) The transgenic cells according to claim 24, wherein said DNA sequence is modified to enhance expression in plant cells.

26. (currently amended) The transgenic cells according to claim 24, further comprising a chloroplast transit peptide adapted to target the NADP-GDH enzyme to the chloroplasts.

27. (original) The transgenic cells according to claim 24, wherein said transcription initiation region is constitutive in action.

28. (original) The transgenic cells according to claim 24, wherein said transcription initiation region is tissue specific.

29. (original) The transgenic cells according to claim 28, wherein said tissue specific transcription initiation region is seed specific.